

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA

(ii) TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
(AS AMENDED)

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Klauber & Jackson
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- (C) CITY: Hackensack
- (D) STATE: New Jersey
- (E) COUNTRY: USA
- (F) ZIP: 07601

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/204,730
- (B) FILING DATE: December 3, 1998
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/292,345
- (B) FILING DATE: August 17, 1994
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Jackson Esq., David A.
- (B) REGISTRATION NUMBER: 26,742
- (C) REFERENCE/DOCKET NUMBER: 600-1-087DIV

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: Murine ob cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mus musculus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAGCAGCTG CAAGGTGCAA GAAGAAGAAG ATCCCAGGGA CGAAAATGTG CTGGAGACCC	60
CTGTGTCGGN TTCTGTGGC TTTGGTCCTA TCTGTCTTAT GTTCAAGCAG TGCCTATCCA	120
GAAAGTCCAG GATGACACCA AAACCCTCAT CAAGACCATT GTCACCAGGA TCAATGACAT	180
TTCACACACG CAGTCGGTAT CCGCCAAGCA GAGGGTCACT GGCTTGGACT TCATTCTGG	240
GCTTCACCCCC ATTCTGAGTT TGTCCAAGAT GGACCAGACT CTGGCAGTCT ATCAACAGGT	300
CCTCACCCAGC CTGCCTTCCC AAAATGTGCT GCAGATAGCC AATGACCTGG AGAATCTCCG	360
AGACCTCCTC CATCTGCTGG CCTTCTCCAA GAGCTGCTCC CTGCCTCAGA CCAGTGGCCT	420
GCAGAAGCCA GAGAGCCTGG ATGGCGTCCT GGAAGCCTCA CTCTACTCCA CAGAGGTGGT	480
GGCTTGAGC AGGCTGCAGG GCTCTCTGCA GGACATTCTT CAACAGTTGG ATGTTAGCCC	540
TGAATGCTGA AGTTTCAAAG GCCACNCAGG CTCCCAAGAA TCATGTAGAG GGAAGAAACC	600
TTGGCTTCCA GGGGTCTTCA GGANNGAAGA GNAGCNCATG TGCACACNNN ATCCANNNT	660
CATTCANTTT CTCTCCCTCC TGTAGACCAC NNNNCCATNN N	701

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(A) DESCRIPTION: Murine ob polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu			
1	5	10	15
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys			
20	25	30	
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr			
35	40	45	
Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro			
50	55	60	
Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala			
65	70	75	80
Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln			
85	90	95	

Ile	Ala	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Leu	Leu	Ala
100								105					110		
Phe	Ser	Lys	Ser	Cys	Ser	Leu	Pro	Gln	Thr	Ser	Gly	Leu	Gln	Lys	Pro
115						120						125			
Glu	Ser	Leu	Asp	Gly	Val	Leu	Glu	Ala	Ser	Leu	Tyr	Ser	Thr	Glu	Val
130						135					140				
Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Ile	Leu	Gln	Gln
145						150				155			160		
Leu	Asp	Val	Ser	Pro	Glu	Cys									
						165									

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 46..546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NNNGNNNGTTG	CAAGGCCCAA	GAAGCCANN	NTCCTGGGAA	GGAAA	ATG	CAT	TGG								54	
								Met	His	Trp						
								1								
GGA	ACC	CTG	TGC	GGA	TTC	TTG	TGG	CTT	TGG	CCC	TAT	CTT	TTC	TAT	GTC	102
Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu	Phe	Tyr	Val	
5						10				15						
CAA	GCT	GTG	CCC	ATC	CAA	AAA	GTC	CAA	GAT	GAC	ACC	AAA	ACC	CTC	ATC	150
Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile	
20						25				30			35			
AAG	ACA	ATT	GTC	ACC	AGG	ATC	AAT	GAC	ATT	TCA	CAC	ACG	CAG	TCA	GTC	198
Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	Gln	Ser	Val	
									40		45		50			
TCC	TCC	AAA	CAG	AAA	GTC	ACC	GGT	TTG	GAC	TTC	ATT	CCT	GGG	CTC	CAC	246
Ser	Ser	Lys	Lys	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly	Leu	His		
									55		60		65			

CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln	70	75	80	294
CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn	85	90	95	342
GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys	100	105	110	390
AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu	120	125	130	438
GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu	135	140	145	486
AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu	150	155	160	534
AGC CCT GGG TGC TGAGGCCTT GAAGGTCACT CTTCTGCAA GGACTNACGT Ser Pro Gly Cys	165			585
TAAGGGAAGG AACTCTGGTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC				645
CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTTTCC AAAGG				700

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 - (A) DESCRIPTION: Human ob polypeptide
- (vi) ORIGINAL SOURCE: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu	1	5	10	15
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys	20	25	30	
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr	35	40	45	
Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro	50	55	60	
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala	65	70	75	80

Val	Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Met	Pro	Ser	Arg	Asn	Val	Ile	Gln
				85						90					95
Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala
				100				105						110	
Phe	Ser	Lys	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu
				115				120						125	
Asp	Ser	Leu	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val
				130			135						140		
Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln
				145			150			155				160	
Leu	Asp	Leu	Ser	Pro	Gly	Cys									
				165											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide lacking Gln at position

49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Cys	Trp	Arg	Pro	Leu	Cys	Arg	Phe	Leu	Trp	Leu	Trp	Ser	Tyr	Leu
1				5					10					15	
Ser	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys
				20					25					30	
Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr
				35				40					45		
Ser	Val	Ser	Ala	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly
				50			55						60		
Leu	His	Pro	Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	Val
				65			70			75				80	
Tyr	Gln	Gln	Val	Leu	Thr	Ser	Leu	Pro	Ser	Gln	Asn	Val	Leu	Gln	Ile
				85					90					95	
Ala	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Leu	Leu	Ala	Phe
				100				105						110	

Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu
 115 120 125

Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
 130 135 140

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu
 145 150 155 160

Asp Val Ser Pro Glu Cys -
 165

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) Description: Human ob polypeptide lacking Gln at position

49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
1 5 10 15

Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30

Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45

Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
50 55 60

Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val
65 70 75 80

Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
85 90 95

Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
100 105 110

Ser Ileu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val
130 135 140

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu
145 150 155 160

Asp Leu Ser Pro Gly Cys
165

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: PCR 5 primer for exon 2G7
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCAGGGCAGG AAAATGTG

18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: PCR 3 primer for exon 2G7
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATCCTGGAC TTTCTGGATA GG

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
 - (A) DESCRIPTION: exon 2G7
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG TGTCGGGTCC	60
NGTGGNTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC TATCCAGAAA GTCCAGGATG	120
ACACCAAAAG CCTCATCAAG ACCATTGTCA NCAGGATCAC TGANATTCA CACACG	176

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (A) DESCRIPTION: putative N-terminal signal sequence of Murine Ob Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Phe leu trp leu trp ser tyr leu ser tyr val gln ala val pro			
1	5	10	15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (plasmid)

- (A) DESCRIPTION: pET-15b expression vector

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: T7 promoter
- (B) LOCATION: 20..37

(ix) FEATURE:

- (A) NAME/KEY: lac operator
- (B) LOCATION: 39..64

(ix) FEATURE:

- (A) NAME/KEY: His-Tag
- (B) LOCATION: 123..137

(ix) FEATURE:

- (A) NAME/KEY: Thrombin cleavage site
- (B) LOCATION: 184..196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60		
TTCCCCCTCTA CAAATAATT TGTTTAACCT TAAGAAGGAG ATATACC ATG GGC AGC	116		
1			
AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG CGC GGC AGC	164		
5	10	15	
CAT ATG CTC GAG GAT CCC GCT GCT AAC AAA GCC CGA AAG GAA GCT GAG	212		
20	25	30	35
TTG GCT GCT GCC ACC GCT GAG CAA TAA CTA G CATAACCCCT TGGGGCCTCT	263		
40			
AAACGGGTCT TGAGGGTTT TTTG	287		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Murine 5' primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTTATGTTCA TATGGTGCCG ATCCAGAAAG TC	32
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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Murine 3' primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCCCTCTACA TATGTCTTGG GAGCCTGGTG GC

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Human 5 primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCTATGTCCA TATGGTGCCG ATCCAAAAAG TC

32

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Human 3 primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCCTTCCCA TATGGTACTC CTTGCAGGAA GA 32

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) DESCRIPTION: Splice acceptor site in ob

(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
(A) NAME/KEY: Splice acceptor site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGCAGTCGGT A

11

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(A) DESCRIPTION: abnormal splice acceptor site in ob

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: No

(ix) FEATURE:
(A) NAME/KEY: Splice acceptor site (without Glutamine)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AG CAG TCG GTA

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE: -
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
 (A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Leu Asp

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
 (A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: Carboxyl terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Pro Glu Cys
20